Qiong Yang

List of Publications by Year in Descending Order

121 papers	12,015 citations	49 h-index	109 g-index
133 ext. papers	15,680 ext. citations	11.5 avg, IF	4.9 L-index

#	Paper	IF	Citations
121	Genome-wide association study reveals novel genetic loci: a new polygenic risk score for mitral valve prolapse.. *European Heart Journal*, **2022**,	9.5	2
120	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
119	New insights into the genetic etiology of Alzheimer's disease and related dementias.. *Nature Genetics*, **2022**,	36.3	27
118	Associations Between Brainstem Volume and Alzheimer's Disease Pathology in Middle-Aged Individuals of the Framingham Heart Study.. *Journal of Alzheimer's Disease*, **2022**,	4.3	
117	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
116	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
115	Proteomic profiling reveals biomarkers and pathways in type 2 diabetes risk. *JCI Insight*, **2021**, 6,	9.9	6
114	Multiomics integrative analysis identifies allele-specific blood biomarkers associated to Alzheimer's disease etiopathogenesis. *Aging*, **2021**, 13, 9277-9329	5.6	4
113	Multiomic Profiling in Black and White Populations Reveals Novel Candidate Pathways in Left Ventricular Hypertrophy and Incident Heart Failure Specific to Black Adults. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003191	5.2	2
112	Plasma amyloid β levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genome-wide association study in over 12,000 non-demented participants. *Alzheimer's and Dementia*, **2021**, 17, 1663-1674	1.2	5
111	Allele-specific DNA methylation maps in monozygotic twins discordant for psychiatric disorders reveal that disease-associated switching at the EIPR1 regulatory loci modulates neural function. *Molecular Psychiatry*, **2021**,	15.1	1
110	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. *Nature Communications*, **2021**, 12, 3417	17.4	23
109	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. *Kidney International*, **2021**, 99, 926-939	9.9	6
108	Proteomic Signatures of Lifestyle Risk Factors for Cardiovascular Disease: A Cross-Sectional Analysis of the Plasma Proteome in the Framingham Heart Study. *Journal of the American Heart Association*, **2021**, 10, e018020	6	3
107	An evaluation of approaches for rare variant association analyses of binary traits in related samples. *Scientific Reports*, **2021**, 11, 3145	4.9	1
106	The genetics of circulating BDNF: towards understanding the role of BDNF in brain structure and function in middle and old ages. *Brain Communications*, **2020**, 2, fcaa176	4.5	1
105	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. *Circulation: Heart Failure*, **2020**, 13, e006749	7.6	8

104	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. *Stroke*, **2020**, 51, 2111-2121	6.7	23
103	The genetic architecture of the human cerebral cortex. *Science*, **2020**, 367,	33.3	156
102	Genetic Architecture of Circulating Very-Long-Chain (C24:0 and C22:0) Ceramide Concentrations. *Journal of Lipid and Atherosclerosis*, **2020**, 9, 172-183	3	6
101	Proteomic Profiling in Biracial Cohorts Implicates DC-SIGN as a Mediator of Genetic Risk in COVID-19 **2020**,		14
100	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. *Nature Communications*, **2020**, 11, 4796	17.4	16
99	Circulating testican-2 is a podocyte-derived marker of kidney health. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 25026-25035	11.5	7
98	Exome Array Analysis of Early-Onset Ischemic Stroke. *Stroke*, **2020**, 51, 3356-3360	6.7	1
97	Association of common genetic variants with brain microbleeds: A genome-wide association study. *Neurology*, **2020**, 95, e3331-e3343	6.5	10
96	Association of circulating metabolites in plasma or serum and risk of stroke: Meta-analysis from seven prospective cohorts. *Neurology*, **2020**,	6.5	9
95	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
94	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
93	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
92	Proteomics Profiling and Risk of New-Onset Atrial Fibrillation: Framingham Heart Study. *Journal of the American Heart Association*, **2019**, 8, e010976	6	24
91	Association of variants in HTRA1 and NOTCH3 with MRI-defined extremes of cerebral small vessel disease in older subjects. *Brain*, **2019**, 142, 1009-1023	11.2	21
90	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. *Communications Biology*, **2019**, 2, 285	6.7	14
89	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
88	Profiling of the plasma proteome across different stages of human heart failure. *Nature Communications*, **2019**, 10, 5830	17.4	25
87	Genetic architecture of subcortical brain structures in 38,851 individuals. *Nature Genetics*, **2019**, 51, 1624-1636	36.3	81

86	Genetic Architecture of the Cardiovascular Risk Proteome. *Circulation*, **2018**, 137, 1158-1172	16.7	47
85	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. *Alzheimer's and Dementia*, **2018**, 14, 707-722	1.2	76
84	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. *Stroke*, **2018**, 49, 1812-1819	6.7	10
83	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
82	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. *Nature Communications*, **2018**, 9, 3945	17.4	16
81	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. *Circulation*, **2018**, 138, 2469-2481	16.7	23
80	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. *Nature Communications*, **2018**, 9, 4228	17.4	31
79	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
78	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
77	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. *Scientific Reports*, **2017**, 7, 45040	4.9	70
76	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
75	Heritability of Mitral Regurgitation: Observations From the Framingham Heart Study and Swedish Population. *Circulation: Cardiovascular Genetics*, **2017**, 10,		8
74	Whole exome sequence-based association analyses of plasma amyloid-β in African and European Americans; the Atherosclerosis Risk in Communities-Neurocognitive Study. *PLoS ONE*, **2017**, 12, e0180046	2.7	6
73	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508
72	Epigenome-wide association studies identify DNA methylation associated with kidney function. *Nature Communications*, **2017**, 8, 1286	17.4	92
71	Genetic risk score and risk of stage 3 chronic kidney disease. *BMC Nephrology*, **2017**, 18, 32	2.7	15
70	Dimethylguanidino valeric acid is a marker of liver fat and predicts diabetes. *Journal of Clinical Investigation*, **2017**, 127, 4394-4402	15.9	71
69	An exome array study of the plasma metabolome. *Nature Communications*, **2016**, 7, 12360	17.4	47

68	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. *Diabetes*, **2016**, 65, 803-17	0.9	96
67	Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 67, 407-416	15.1	101
66	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
65	RVFam: an R package for rare variant association analysis with family data. *Bioinformatics*, **2016**, 32, 624-6	7.2	7
64	Association of Alzheimer's disease GWAS loci with MRI markers of brain aging. *Neurobiology of Aging*, **2015**, 36, 1765.e7-1765.e16	5.6	63
63	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. *Circulation: Cardiovascular Genetics*, **2015**, 8, 398-409		119
62	Gene-centric approach identifies new and known loci for FVIII activity and VWF antigen levels in European Americans and African Americans. *American Journal of Hematology*, **2015**, 90, 534-40	7.1	15
61	Lipid and lipoprotein measurements and the risk of ischemic vascular events: Framingham Study. *Neurology*, **2015**, 84, 472-9	6.5	43
60	A genetic association study of D-dimer levels with 50K SNPs from a candidate gene chip in four ethnic groups. *Thrombosis Research*, **2014**, 134, 462-7	8.2	5
59	Genome-wide meta-analysis of homocysteine and methionine metabolism identifies five one carbon metabolism loci and a novel association of ALDH1L1 with ischemic stroke. *PLoS Genetics*, **2014**, 10, e1004214	6	57
58	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
57	Common variants in Mendelian kidney disease genes and their association with renal function. *Journal of the American Society of Nephrology: JASN*, **2013**, 24, 2105-17	12.7	27
56	A combined epidemiologic and metabolomic approach improves CKD prediction. *Journal of the American Society of Nephrology: JASN*, **2013**, 24, 1330-8	12.7	172
55	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. *Blood*, **2012**, 120, 4873-81	2.2	65
54	Association of genetic variation in the mitochondrial genome with blood pressure and metabolic traits. *Hypertension*, **2012**, 60, 949-56	8.5	30
53	Using family-based imputation in genome-wide association studies with large complex pedigrees: the Framingham Heart Study. *PLoS ONE*, **2012**, 7, e51589	3.7	10
52	Flexible semiparametric analysis of longitudinal genetic studies by reduced rank smoothing. *Journal of the Royal Statistical Society Series C: Applied Statistics*, **2012**, 61, 1-24	1.5	15
51	Genome-wide association and functional follow-up reveals new loci for kidney function. *PLoS Genetics*, **2012**, 8, e1002584	6	143

50	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. *Human Molecular Genetics*, **2012**, 21, 5329-43	5.6	54
49	Methods for Analyzing Multivariate Phenotypes in Genetic Association Studies. *Journal of Probability and Statistics*, **2012**, 2012, 652569	0.6	68
48	Association of estimated glomerular filtration rate and urinary uromodulin concentrations with rare variants identified by UMOD gene region sequencing. *PLoS ONE*, **2012**, 7, e38311	3.7	21
47	Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate Gene Association Resource (CARe). *Blood*, **2011**, 117, 268-75	2.2	31
46	A comparison of strategies for analyzing dichotomous outcomes in genome-wide association studies with general pedigrees. *Genetic Epidemiology*, **2011**, 35, 650-7	2.6	12
45	CUBN is a gene locus for albuminuria. *Journal of the American Society of Nephrology: JASN*, **2011**, 22, 555-70	12.7	170
44	Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. *Human Molecular Genetics*, **2011**, 20, 4056-68	5.6	86
43	Identification of cis- and trans-acting genetic variants explaining up to half the variation in circulating vascular endothelial growth factor levels. *Circulation Research*, **2011**, 109, 554-63	15.7	57
42	Genetic predictors of fibrin D-dimer levels in healthy adults. *Circulation*, **2011**, 123, 1864-72	16.7	47
41	Association of eGFR-Related Loci Identified by GWAS with Incident CKD and ESRD. *PLoS Genetics*, **2011**, 7, e1002292	6	144
40	Assessment of genetic determinants of the association of fibrinogen in relation to cardiovascular disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2011**, 31, 2345-52	9.4	37
39	New loci associated with kidney function and chronic kidney disease. *Nature Genetics*, **2010**, 42, 376-84	36.3	599
38	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. *Nature Genetics*, **2010**, 42, 608-13	36.3	204
37	Clinical and genetic correlates of circulating angiopoietin-2 and soluble Tie-2 in the community. *Circulation: Cardiovascular Genetics*, **2010**, 3, 300-6		39
36	Association of single nucleotide polymorphisms on chromosome 9p21.3 with platelet reactivity: a potential mechanism for increased vascular disease. *Circulation: Cardiovascular Genetics*, **2010**, 3, 445-53		48
35	GWAF: an R package for genome-wide association analyses with family data. *Bioinformatics*, **2010**, 26, 580-1	7.2	195
34	Candidate gene association resource (CARe): design, methods, and proof of concept. *Circulation: Cardiovascular Genetics*, **2010**, 3, 267-75		125
33	Genome-wide association studies of serum magnesium, potassium, and sodium concentrations identify six Loci influencing serum magnesium levels. *PLoS Genetics*, **2010**, 6, e1001045	6	144

32	Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors. *Circulation: Cardiovascular Genetics*, **2010**, 3, 523-30		243
31	Analyze multivariate phenotypes in genetic association studies by combining univariate association tests. *Genetic Epidemiology*, **2010**, 34, 444-54	2.6	113
30	A three-stage approach for genome-wide association studies with family data for quantitative traits. *BMC Genetics*, **2010**, 11, 40	2.6	3
29	Association of novel genetic Loci with circulating fibrinogen levels: a genome-wide association study in 6 population-based cohorts. *Circulation: Cardiovascular Genetics*, **2009**, 2, 125-33		77
28	Common variants at 30 loci contribute to polygenic dyslipidemia. *Nature Genetics*, **2009**, 41, 56-65	36.3	1095
27	Multiple loci associated with indices of renal function and chronic kidney disease. *Nature Genetics*, **2009**, 41, 712-7	36.3	469
26	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nature Genetics*, **2009**, 41, 1191-8	36.3	285
25	CDKN1C/p57kip2 is a candidate tumor suppressor gene in human breast cancer. *BMC Cancer*, **2008**, 8, 68	4.8	46
24	Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. *Lancet, The*, **2008**, 372, 1953-61	40	520
23	Handling linkage disequilibrium in linkage analysis using dense single-nucleotide polymorphisms. *BMC Proceedings*, **2007**, 1 Suppl 1, S161	2.3	6
22	Evidence for linkage of red blood cell size and count: genome-wide scans in the Framingham Heart Study. *American Journal of Hematology*, **2007**, 82, 605-10	7.1	29
21	Using linkage and association to identify and model genetic effects: summary of GAW15 Group 4. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S34-42	2.6	3
20	Effect of linkage disequilibrium between markers in linkage and association analyses. *Genetic Epidemiology*, **2007**, 31 Suppl 1, S139-48	2.6	1
19	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S1	2.1	152
18	A genome-wide association for kidney function and endocrine-related traits in the NHLBI's Framingham Heart Study. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S10	2.1	71
17	Genome-wide association and linkage analyses of hemostatic factors and hematological phenotypes in the Framingham Heart Study. *BMC Medical Genetics*, **2007**, 8 Suppl 1, S12	2.1	60
16	The Third Generation Cohort of the National Heart, Lung, and Blood Institute's Framingham Heart Study: design, recruitment, and initial examination. *American Journal of Epidemiology*, **2007**, 165, 1328-35	3.8	605
15	Joint modeling of linkage and association using affected sib-pair data. *BMC Proceedings*, **2007**, 1 Suppl 1, S38	2.3	3

14	Maternal influence on blood pressure suggests involvement of mitochondrial DNA in the pathogenesis of hypertension: the Framingham Heart Study. *Journal of Hypertension*, **2007**, 25, 2067-73	1.9	41
13	Common genetic variation in five thrombosis genes and relations to plasma hemostatic protein level and cardiovascular disease risk. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2006**, 26, 1405-12	9.4	53
12	Genome-wide search for genes affecting serum uric acid levels: the Framingham Heart Study. *Metabolism: Clinical and Experimental*, **2005**, 54, 1435-41	12.7	83
11	Genome-wide linkage analysis to urinary microalbuminuria in a community-based sample: the Framingham Heart Study. *Kidney International*, **2005**, 67, 70-4	9.9	40
10	Genome-wide linkage analyses and candidate gene fine mapping for HDL3 cholesterol: the Framingham Study. *Journal of Lipid Research*, **2005**, 46, 1416-25	6.3	21
9	Comprehensive survey of common genetic variation at the plasminogen activator inhibitor-1 locus and relations to circulating plasminogen activator inhibitor-1 levels. *Circulation*, **2005**, 112, 1728-35	16.7	63
8	Genomewide linkage analysis to serum creatinine, GFR, and creatinine clearance in a community-based population: the Framingham Heart Study. *Journal of the American Society of Nephrology: JASN*, **2004**, 15, 2457-61	12.7	141
7	Quantitative DNA fingerprinting may distinguish new primary breast cancer from disease recurrence. *Journal of Clinical Oncology*, **2004**, 22, 1830-8	2.2	42
6	Description of the Framingham Heart Study data for Genetic Analysis Workshop 13. *BMC Genetics*, **2003**, 4 Suppl 1, S2	2.6	19
5	Genetic analyses of longitudinal phenotype data: a comparison of univariate methods and a multivariate approach. *BMC Genetics*, **2003**, 4 Suppl 1, S29	2.6	8
4	A genome-wide search for genes affecting circulating fibrinogen levels in the Framingham Heart Study. *Thrombosis Research*, **2003**, 110, 57-64	8.2	25
3	Genetic variants for head size share genes and pathways with cancer		2
2	New insights on the genetic etiology of Alzheimer's and related dementia		25
1	Genetic Determinants of Cortical Structure (Thickness, Surface Area and Volumes) among Disease Free Adults in the CHARGE Consortium		7